FIG. 1

```
AQSVPYGVSQIKAPALHSQGYTGSNVKVAV
1         10        20        30
IDSGIDSSHPDLKVAGGASMVPSETNPFQDNN
          40        50        60
SHGTHVAGTVAALNNSIGVLGVAPSASLYAVK
          70        80        90
VLGADGSGQYSWIINGIEWAIANNMDVINMSL
         100       110       120
GGPSGSAALKAAVDKAVASGVVVVAAAGNEG
     130       140       150
TSGSSSTVGYPGKYPSVIAVGAVDSSNQRASF
   160       170       180
SSVGPELDVMAPGVSIQSTLPGNKYGAYNGTS
190       200       210       220
MASPHVAGAAALILSKHPNWTNTQVRSSLENT
          230       240       250
TTKLGDSFYYGKGLINVQAAAQ
         260       270
```

FIG. 2

GCGCAGTCCGTGCCTTACGGCGTATCACAAATTAAAGCCCCTGCTC
TGCACTCTCAAGGCTACACTGGATCAAATGTTAAAGTAGCGGTTAT
CGACAGCGGTATCGATTCTTCTCATCCTGATTTAAAGGTAGCAGGC
GGAGCCAGCATGGTTCCTTCTGAAACAAATCCTTTCCAAGACAAC
AACTCTCACGGAACTCACGTTGCCGGCACAGTTGCGGCTCTTAATA
ACTCAATCGGTGTATTAGGCGTTGCGCCAAGCGCATCACTTTACGC
TGTAAAAGTTCTCGGTGCTGACGGTTCCGGCCAATACAGCTGGATC
ATTAACGGAATCGAGTGGGCGATCGCAAACAATATGGACGTTATT
AACATGAGCCTCGGCGGACCTTCTGGTTCTGCTGCTTTAAAAGCGG
CAGTTGATAAAGCCGTTGCATCCGGCGTCGTAGTCGTTGCGGCAGC
CGGTAACGAAGGCACTTCCGGCAGCTCAAGCACAGTGGGCTACCC
TGGTAAATACCCTTCTGTCATTGCAGTAGGCGCTGTTGACAGCAGC
AACCAAAGAGCATCTTTCTCAAGCGTAGGACCTGAGCTTGATGTC
ATGGCACCTGGCGTATCTATCCAAAGCACGCTTCCTGGAAACAAA
TACGGGGCGTACAACGGTACGTCAATGGCATCTCCGCACGTTGCC
GGAGCGGCTGCTTTGATTCTTTCTAAGCACCCGAACTGGACAAACA
CTCAAGTCCGCAGCAGTTTAGAAAACACCACTACAAAACTTGGTG
ATTCTTTCTACTATGGAAAAGGGCTGATCAACGTACAGGCGGCAG
CTCAGTAA

FIG. 3

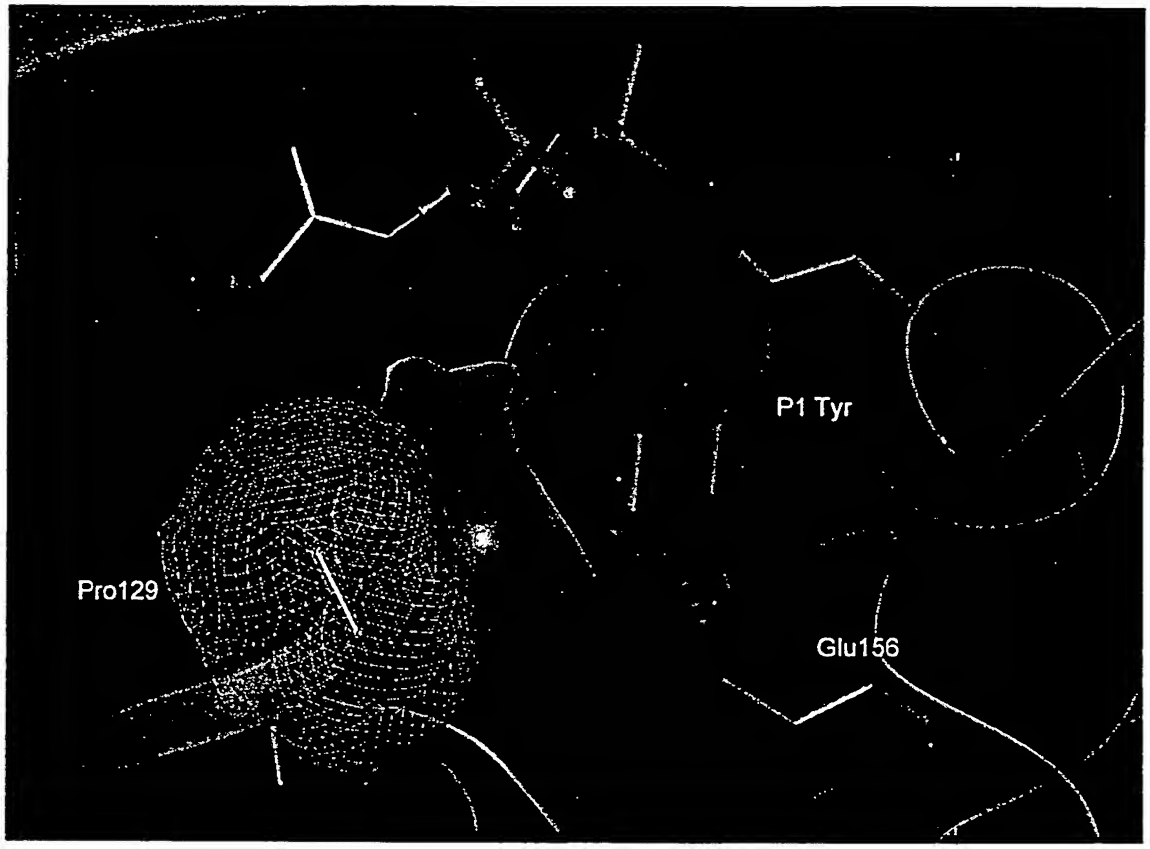


FIG. 4

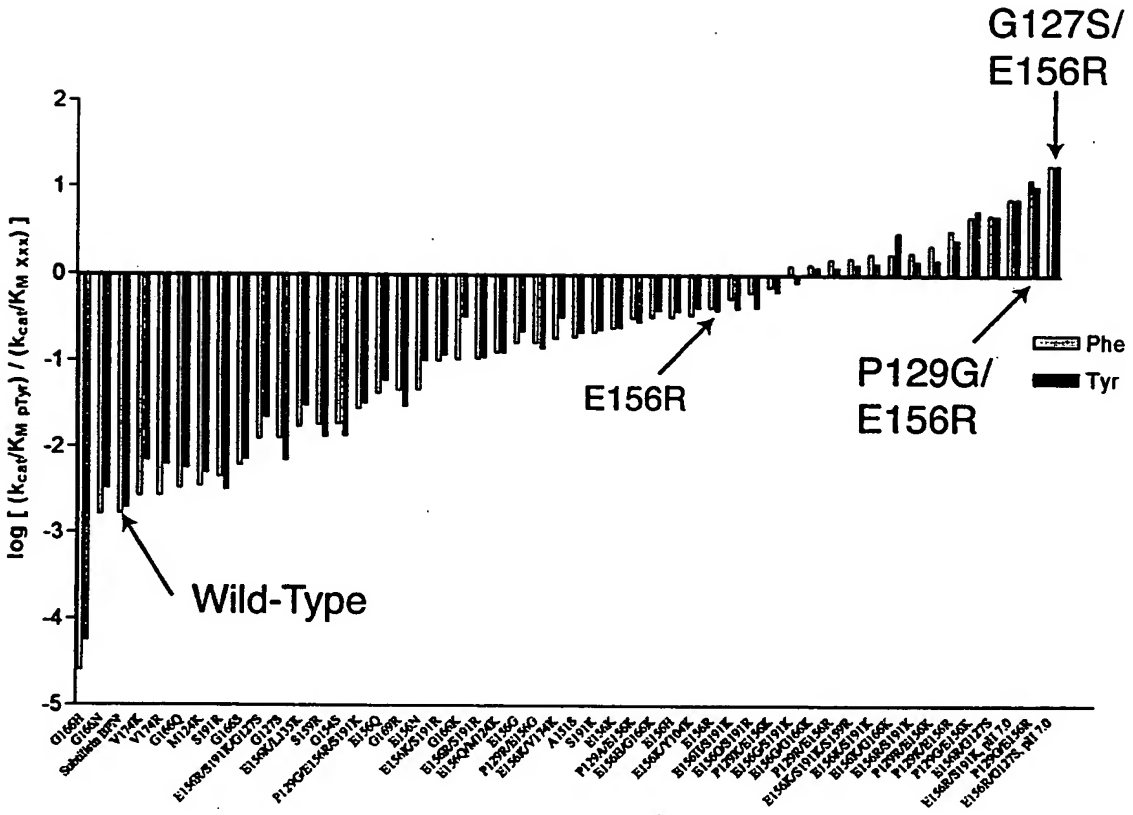
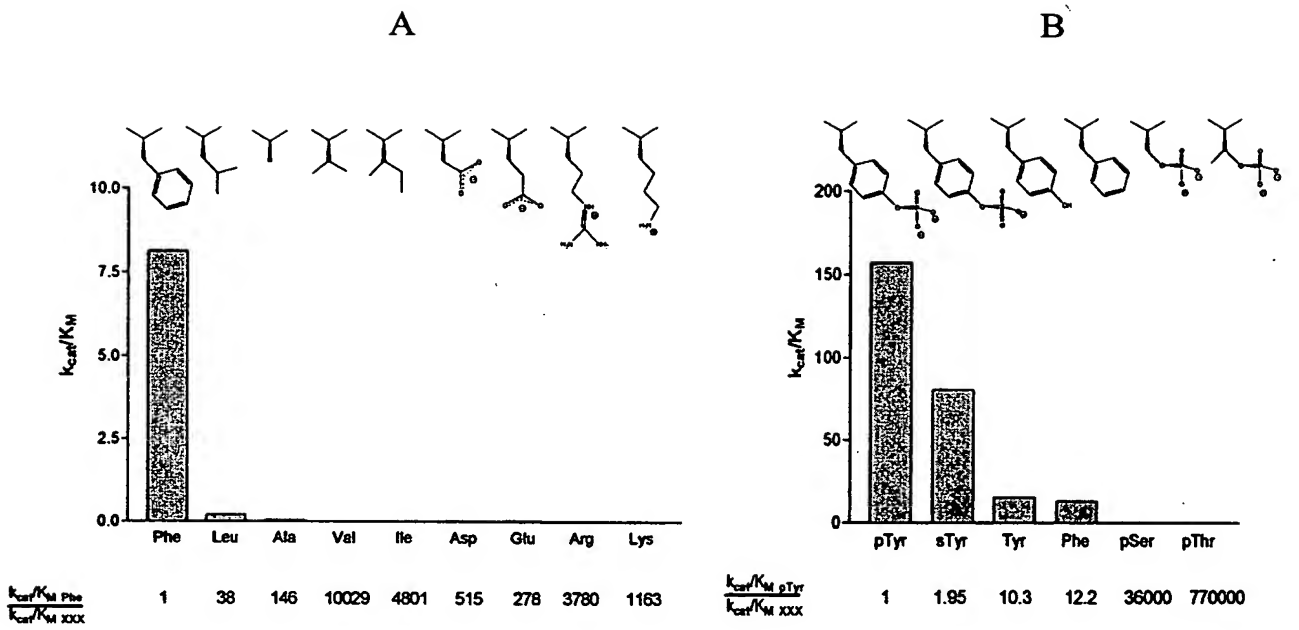


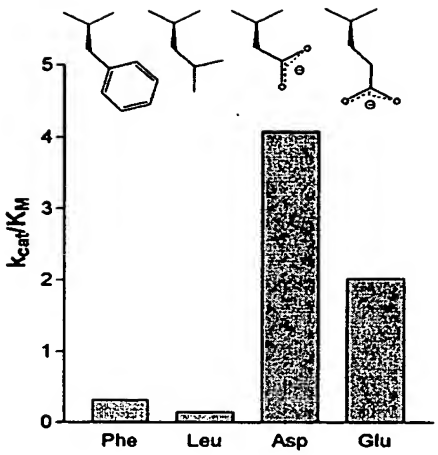
FIG. 5



Suc-Ala-Ala-Pro-Xxx-pNA

Abz-Phe-Arg-Pro-Xxx-Gly-Phe-Y(NO2)-Asp

FIG. 6



$\frac{k_{cat}/K_{M\ Phe}}{k_{cat}/K_{M\ XXX}}$	Phe	Leu	Asp	Glu
	1	2.14	0.078	0.157

FIG. 7

MRGKKVWISLLFALALIFTMAFGSTSSAQAAGKSNGEKKYI
VGFKQTMSTMSAAKKKDVISEKGGKVQKQFKYVDAASATLN
EKAVKELKKDPSVAYVEEDHVAHAYAQSVPYGVSQIKAPALH
SQGYTGSNVKVAVIDSGIDSSHPDLKVAGGASMVPSETNPFQD
NNSHGTHVAGTVAALNNSIGVLGVAPSASLYAVKVLGADGSG
QYSWIINGIEWAIANNMDVINMSLGGPSGSAALKAAVDKAVA
SGVVVVAAAGNEGTSGSSSTVGYPGKYPSVIAVGAVDSSNQR
ASFSSVGPELDVMAPGVSIQSTLPGNKYGAYNGTSMASPHVA
GAAALILSKHPNWTNTQVRSSLENTTTKLGDSFYYGKGLINVQ
AAAQ

FIG. 8

GTGAGAGGCAAAAAAGTATGGATCAGTTTGCTGTTTGC
TTTAGCGTTAATCTTTACGATGGCGTTCGGCAGCACAT
CCTCTGCCCAGGCGGCAGGGAAATCAAACGGGGAAAAG
AAATATATTGTCGGGTTTAAACAGACAATGAGCACGATGA
GCGCCGCTAAGAAGAAAGATGTCATTTCTGAAAAAGGCG
GGAAAGTGCAAAAGCAATTCAAATATGTAGACGCAGCTTC
AGCTACATTAAACGAAAAAGCTGTAAAAGAATTGAAAAA
AGACCCGAGCGTCGCTTACGTTGAAGAAGATCACGTAGCA
CATGCGTACGCGCAGTCCGTGCCTTACGGCGTATCACAAA
TTAAAGCCCCTGCTCTGCACTCTCAAGGCTACACTGGATC
AAATGTTAAAGTAGCGGTTATCGACAGCGGTATCGATTCT
TCTCATCCTGATTTAAAGGTAGCAGGCGGAGCCAGCATGG
TTCCTTCTGAAACAAATCCTTTCCAAGACAACAACTCTCAC
GGAACTCACGTTGCCGGCACAGTTGCGGCTCTTAATAACT
CAATCGGTGTATTAGGCGTTGCGCCAAGCGCATCACTTTA
CGCTGTAAAAGTTCTCGGTGCTGACGGTTCCGGCCAATAC
AGCTGGATCATTAACGGAATCGAGTGGGCGATCGCAAACA
ATATGGACGTTATTAACATGAGCCTCGGCGGACCTTCTGG
TTCTGCTGCTTTAAAAGCGGCAGTTGATAAAGCCGTTGCA
TCCGGCGTCGTAGTCGTTGCGGCAGCCGGTAACGAAGGCA
CTTCCGGCAGCTCAAGCACAGTGGGCTACCCTGGTAAATA
CCCTTCTGTCATTGCAGTAGGCGCTGTTGACAGCAGCAAC
CAAAGAGCATCTTTCTCAAGCGTAGGACCTGAGCTTGATG
TCATGGCACCTGGCGTATCTATCCAAAGCACGCTTCCTGG
AAACAAATACGGGGCGTACAACGGTACGTCAATGGCATCT
CCGCACGTTGCCGGAGCGGCTGCTTTGATTCTTTCTAAGCA
CCCGAACTGGACAAACACTCAAGTCCGCAGCAGTTTAGAA
AACACCACTACAAAACTTGGTGATTCTTTCTACTATGGAA
AAGGGCTGATCAACGTACAGGCGGCAGCTCAGTAA